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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/922,958

DATE: 08/14/2001
TIME: 12:25:37

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ENTERED

3 <110> APPLICANT: POELLINGER, Lorenz
4 PEREIRA, Teresa
5 RUAS, Jorge
7 <120> TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE
FACTOR-1 BY
8 THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
10 <130> FILE REFERENCE: 3743/49008
12 <140> CURRENT APPLICATION NUMBER: US/09/922,958
12 <141> CURRENT FILING DATE: 2001-08-07
12 <150> PRIOR APPLICATION NUMBER: US 60/223,480
13 <151> PRIOR FILING DATE: 2000-08-07
15 <160> NUMBER OF SEQ ID NOS: 7
17 <170> SOFTWARE: PatentIn version 3.0
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21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(639)
28 <400> SEQUENCE: 1
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31 1 5 10 15
33 gag gca ggc gtc gaa gag tac ggc cct gaa gaa gac ggc ggg gag gag 96
34 Glu Ala Gly Val Glu Glu Tyr Gly Pro Glu Glu Asp Gly Gly Glu Glu
35 20 25 30
37 tcg ggc gcc gag gag tcc ggc ccg gaa gag tcc ggc ccg gag gaa ctg 144
38 Ser Gly Ala Glu Glu Ser Gly Pro Glu Glu Ser Gly Pro Glu Glu Leu
39 35 40 45
41 ggc gcc gag gag gag atg gag gcc ggc ccg ccg ccg gtc ctg ctg cgc 192
42 Gly Ala Glu Glu Glu Met Glu Ala Gly Arg Pro Arg Pro Val Leu Arg
43 50 55 60
45 tcg gtg aac tcg cgc gag ccc tcc cag gtc atc ttc tgc aat cgc agt 240
46 Ser Val Asn Ser Arg Glu Pro Ser Gln Val Ile Phe Cys Asn Arg Ser
47 65 70 75 80
49 ccg cgc gtc gtg ctg ccc gta tgg ctc aac ttc gac ggc gag ccg cag 288
50 Pro Arg Val Val Leu Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln
51 85 90 95
53 ccc tac cca acg ctg ccg cct ggc acg ggc cgc cgc atc cac agc tac 336
54 Pro Tyr Pro Thr Leu Pro Pro Gly Thr Gly Arg Arg Ile His Ser Tyr
55 100 105 110
57 cga ggt cac ctt tgg ctc ttc aga gat gca ggg aca cac gat ggg ctt 384
58 Arg Gly His Leu Trp Leu Phe Arg Asp Ala Gly Thr His Asp Gly Leu
59 115 120 125
61 ctg gtt aac caa act gaa tta ttt gtg cca tct ctc aat gtt gac gga 432
62 Leu Val Asn Gln Thr Glu Leu Phe Val Pro Ser Leu Asn Val Asp Gly
63 130 135 140

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67 145      150      155      160
69 cga tgc ctc cag gtt gtc cgg agc cta gtc aag cct gag aat tac agg      528
70 Arg Cys Leu Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn Tyr Arg
71      165      170      175
73 aga ctg gac atc gtc agg tcg ctc tac gaa gat ctg gaa gac cac cca      576
74 Arg Leu Asp Ile Val Arg Ser Leu Tyr Glu Asp Leu Glu Asp His Pro
75      180      185      190
77 aat gtg cag aaa gac ctg gag cgg ctg aca cag gag cgc att gca cat      624
78 Asn Val Gln Lys Asp Leu Glu Arg Leu Thr Gln Glu Arg Ile Ala His
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81 caa cgg atg gga gat tga      642
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88 <212> TYPE: PRT
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101 Ser Gly Ala Glu Glu Ser Gly Pro Glu Glu Ser Gly Pro Glu Glu Leu
102      35      40      45
105 Gly Ala Glu Glu Glu Met Glu Ala Gly Arg Pro Arg Pro Val Leu Arg
106      50      55      60
109 Ser Val Asn Ser Arg Glu Pro Ser Gln Val Ile Phe Cys Asn Arg Ser
110 65      70      75      80
113 Pro Arg Val Val Leu Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln
114      85      90      95
117 Pro Tyr Pro Thr Leu Pro Pro Gly Thr Gly Arg Arg Ile His Ser Tyr
118      100      105      110
121 Arg Gly His Leu Trp Leu Phe Arg Asp Ala Gly Thr His Asp Gly Leu
122      115      120      125
125 Leu Val Asn Gln Thr Glu Leu Phe Val Pro Ser Leu Asn Val Asp Gly
126      130      135      140
129 Gln Pro Ile Phe Ala Asn Ile Thr Leu Pro Val Tyr Thr Leu Lys Glu
130 145      150      155      160
133 Arg Cys Leu Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn Tyr Arg
134      165      170      175
137 Arg Leu Asp Ile Val Arg Ser Leu Tyr Glu Asp Leu Glu Asp His Pro
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145 Gln Arg Met Gly Asp
146      210
149 <210> SEQ ID NO: 3

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150 <211> LENGTH: 2481
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155 <221> NAME/KEY: CDS
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163 cgt cga aaa gaa aag tct cga gat gca gcc aga tct cgg cga agt aaa      96
164 Arg Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys
165      20      25      30
167 gaa tct gaa gtt ttt tat gag ctt gct cat cag ttg cca ctt cca cat      144
168 Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His
169      35      40      45
171 aat gtg agt tcg cat ctt gat aag gcc tct gtg atg agg ctt acc atc      192
172 Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile
173      50      55      60
175 agc tat ttg cgt gtg agg aaa ctt ctg gat gct ggt gat ttg gat att      240
176 Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile
177 65      70      75      80
179 gaa gat gac atg aaa gca cag atg aat tgc ttt tat ttg aaa gcc ttg      288
180 Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu
181      85      90      95
183 gat ggt ttt gtt atg gtt ctc aca gat gat ggt gac atg att tac att      336
184 Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile
185      100      105      110
187 tct gat aat gtg aac aaa tac atg gga tta act cag ttt gaa cta act      384
188 Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
189      115      120      125
191 gga cac agt gtg ttt gat ttt act cat cca tgt gac cat gag gaa atg      432
192 Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met
193      130      135      140
195 aga gaa atg ctt aca cac aga aat ggc ctt gtg aaa aag ggt aaa gaa      480
196 Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu
197 145      150      155      160
199 caa aac aca cag cga agc ttt ttt ctc aga atg aag tgt acc cta act      528
200 Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr
201      165      170      175
203 agc cga gga aga act atg aac ata aag tct gca aca tgg aag gta ttg      576
204 Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu
205      180      185      190
207 cac tgc aca ggc cac att cac gta tat gat acc aac agt aac caa cct      624
208 His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro
209      195      200      205
211 cag tgt ggg tat aag aaa cca cct atg acc tgc ttg gtg ctg att tgt      672
212 Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys
213      210      215      220

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215	gaa	ccc	att	cct	cac	cca	tca	aat	att	gaa	att	cct	tta	gat	agc	aag	720
216	Glu	Pro	Ile	Pro	His	Pro	Ser	Asn	Ile	Glu	Ile	Pro	Leu	Asp	Ser	Lys	
217	225					230				235							240
219	act	ttc	ctc	agt	cga	cac	agc	ctg	gat	atg	aaa	ttt	tct	tat	tgt	gat	768
220	Thr	Phe	Leu	Ser	Arg	His	Ser	Leu	Asp	Met	Lys	Phe	Ser	Tyr	Cys	Asp	
221					245				250							255	
223	gaa	aga	att	acc	gaa	ttg	atg	gga	tat	gag	cca	gaa	gaa	ctt	tta	ggc	816
224	Glu	Arg	Ile	Thr	Glu	Leu	Met	Gly	Tyr	Glu	Pro	Glu	Glu	Leu	Leu	Gly	
225				260					265					270			
227	cgc	tca	att	tat	gaa	tat	tat	cat	gct	ttg	gac	tct	gat	cat	ctg	acc	864
228	Arg	Ser	Ile	Tyr	Glu	Tyr	Tyr	His	Ala	Leu	Asp	Ser	Asp	His	Leu	Thr	
229		275						280					285				
231	aaa	act	cat	cat	gat	atg	ttt	act	aaa	gga	caa	gtc	acc	aca	gga	cag	912
232	Lys	Thr	His	His	Asp	Met	Phe	Thr	Lys	Gly	Gln	Val	Thr	Thr	Gly	Gln	
233		290				295						300					
235	tac	agg	atg	ctt	gcc	aaa	aga	ggg	gga	tat	gtc	tgg	gtt	gaa	act	caa	960
236	Tyr	Arg	Met	Leu	Ala	Lys	Arg	Gly	Gly	Tyr	Val	Trp	Val	Glu	Thr	Gln	
237	305				310					315						320	
239	gca	act	gtc	ata	tat	aac	acc	aag	aat	tct	caa	cca	cag	tgc	att	gta	1008
240	Ala	Thr	Val	Ile	Tyr	Asn	Thr	Lys	Asn	Ser	Gln	Pro	Gln	Cys	Ile	Val	
241				325				330						335			
243	tgt	gtg	aat	tac	gtt	gtg	agt	ggg	att	att	cag	cac	gac	ttg	att	ttc	1056
244	Cys	Val	Asn	Tyr	Val	Val	Ser	Gly	Ile	Ile	Gln	His	Asp	Leu	Ile	Phe	
245			340					345					350				
247	tcc	ctt	caa	caa	gaa	tgt	gtc	ctt	aaa	ccg	gtt	gaa	tct	tca	gat		1104
248	Ser	Leu	Gln	Thr	Glu	Cys	Val	Leu	Lys	Pro	Val	Glu	Ser	Ser	Asp		
249		355				360					365						
251	atg	aaa	atg	act	cag	cta	ttc	acc	aaa	gtt	gaa	tca	gaa	gat	aca	agt	1152
252	Met	Lys	Met	Thr	Gln	Leu	Phe	Thr	Lys	Val	Glu	Ser	Glu	Asp	Thr	Ser	
253		370				375				380							
255	agc	ctc	ttt	gac	aaa	ctt	aag	aag	gaa	cct	gat	gct	tta	act	ttg	ctg	1200
256	Ser	Leu	Phe	Asp	Lys	Leu	Lys	Lys	Glu	Pro	Asp	Ala	Leu	Thr	Leu	Leu	
257	385				390				395						400		
259	gcc	cca	gcc	gct	gga	gac	aca	atc	ata	tct	tta	gat	ttt	ggc	agc	aac	1248
260	Ala	Pro	Ala	Ala	Gly	Asp	Thr	Ile	Ile	Ser	Leu	Asp	Phe	Gly	Ser	Asn	
261			405					410					415				
263	gac	aca	gaa	act	gat	gac	cag	caa	ctt	gag	gaa	gta	cca	tta	tat	aat	1296
264	Asp	Thr	Glu	Thr	Asp	Asp	Gln	Gln	Leu	Glu	Glu	Val	Pro	Leu	Tyr	Asn	
265			420					425					430				
267	gat	gta	atg	ctc	ccc	tca	ccc	aac	gaa	aaa	tta	cag	aat	ata	aat	ttg	1344
268	Asp	Val	Met	Leu	Pro	Ser	Pro	Asn	Glu	Lys	Leu	Gln	Asn	Ile	Asn	Leu	
269		435					440						445				
271	gca	atg	tct	cca	tta	ccc	acc	gct	gaa	acg	cca	aag	cca	ctt	cga	agt	1392
272	Ala	Met	Ser	Pro	Leu	Pro	Thr	Ala	Glu	Thr	Pro	Lys	Pro	Leu	Arg	Ser	
273		450				455					460						
275	agt	gct	gac	cct	gca	ctc	aat	caa	gaa	gtt	gca	tta	aaa	tta	gaa	cca	1440
276	Ser	Ala	Asp	Pro	Ala	Leu	Asn	Gln	Glu	Val	Ala	Leu	Lys	Leu	Glu	Pro	
277	465				470				475					480			
279	aat	cca	gag	tca	ctg	gaa	ctt	tct	ttt	acc	atg	ccc	cag	att	cag	gat	1488

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281					485					490					495		
283	cag	aca	cct	agt	cct	tcc	gat	gga	agc	act	aga	caa	agt	tca	cct	gag	1536
284	Gln	Thr	Pro	Ser	Pro	Ser	Asp	Gly	Ser	Thr	Arg	Gln	Ser	Ser	Pro	Glu	
285				500					505					510			
287	cct	aat	agt	ccc	agt	gaa	tat	tgt	ttt	tat	gtg	gat	agt	gat	atg	gtc	1584
288	Pro	Asn	Ser	Pro	Ser	Glu	Tyr	Cys	Phe	Tyr	Val	Asp	Ser	Asp	Met	Val	
289			515					520					525				
291	aat	gaa	ttc	aag	ttg	gaa	ttg	gta	gaa	aaa	ctt	ttt	gct	gaa	gac	aca	1632
292	Asn	Glu	Phe	Lys	Leu	Glu	Leu	Val	Glu	Lys	Leu	Phe	Ala	Glu	Asp	Thr	
293		530				535					540						
295	gaa	gca	aag	aac	cca	ttt	tct	act	cag	gac	aca	gat	tta	gac	ttg	gag	1680
296	Glu	Ala	Lys	Asn	Pro	Phe	Ser	Thr	Gln	Asp	Thr	Asp	Leu	Asp	Leu	Glu	
297	545					550				555					560		
299	atg	tta	gct	ccc	tat	atc	cca	atg	gat	gat	gac	ttc	cag	tta	cgt	tcc	1728
300	Met	Leu	Ala	Pro	Tyr	Ile	Pro	Met	Asp	Asp	Asp	Phe	Gln	Leu	Arg	Ser	
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303	ttc	gat	cag	ttg	tca	cca	tta	gaa	agc	agt	tcc	gca	agc	cct	gaa	agc	1776
304	Phe	Asp	Gln	Leu	Ser	Pro	Leu	Glu	Ser	Ser	Ser	Ala	Ser	Pro	Glu	Ser	
305				580					585					590			
307	gca	agt	cct	caa	agc	aca	gtt	aca	gta	ttc	cag	cag	act	caa	ata	caa	1824
308	Ala	Ser	Pro	Gln	Ser	Thr	Val	Thr	Val	Phe	Gln	Gln	Thr	Gln	Ile	Gln	
309			595				600					605					
311	gaa	cct	act	gct	aat	gcc	acc	act	acc	act	gcc	acc	act	gat	gaa	tta	1872
312	Glu	Pro	Thr	Ala	Asn	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Thr	Asp	Glu	Leu	
313		610				615					620						
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320	Ser	Pro	Ser	Pro	Thr	His	Ile	His	Lys	Glu	Thr	Thr	Ser	Ala	Thr	Ser	
321				645					650					655			
323	tca	cca	tat	aga	gat	act	caa	agt	cgg	aca	gcc	tca	cca	aac	aga	gca	2016
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327	gga	aaa	gga	gtc	ata	gaa	cag	aca	gaa	aaa	tct	cat	cca	aga	agc	cct	2064
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331	aac	gtg	tta	tct	gtc	gct	ttg	agt	caa	aga	act	aca	gtt	cct	gag	gaa	2112
332	Asn	Val	Leu	Ser	Val	Ala	Leu	Ser	Gln	Arg	Thr	Thr	Val	Pro	Glu	Glu	
333		690				695					700						
335	gaa	cta	aat	cca	aag	ata	cta	gct	ttg	cag	aat	gct	cag	aga	aag	cga	2160
336	Glu	Leu	Asn	Pro	Lys	Ile	Leu	Ala	Leu	Gln	Asn	Ala	Gln	Arg	Lys	Arg	
337	705					710					715				720		
339	aaa	atg	gaa	cat	gat	ggt	tca	ctt	ttt	caa	gca	gta	gga	att	gga	aca	2208
340	Lys	Met	Glu	His	Asp	Gly	Ser	Leu	Phe	Gln	Ala	Val	Gly	Ile	Gly	Thr	
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343	tta	tta	cag	cag	cca	gac	gat	cat	gca	gct	act	aca	tca	ctt	tct	tgg	2256
344	Leu	Leu	Gln	Gln	Pro	Asp	Asp	His	Ala	Ala	Thr	Thr	Ser	Leu	Ser	Trp	

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:605 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:618 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7